

U.S. Patent No. 6,893,636  
Attorney Docket No. 037003-0275470

WJ

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re U.S. PATENT NUMBER 6,893,636

Issued: May 17, 2005

Mitchell REFF et al.

Group Art Unit: 1644

Application No. 09/019,441

Examiner: Phuong N. Huynh

Filed: February 5, 1998

Title: GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES  
AND USE THEREOF AS THERAPEUTICS

\* \* \* \* \*

**REQUEST FOR CERTIFICATE OF CORRECTION**

**PURSUANT TO 37 C.F.R. § 1.323**

**ATTN: Certificate of Correction Branch**  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

**Certificate**  
JUN 13 2005  
**of Correction**

Sir:

Pursuant to 37 C.F.R. § 1.323, patentee respectfully requests that a Certificate of Correction be issued in the above-identified patent to correct the sequence listing. Specifically, the substitute sequence listing filed in the United States Patent and Trademark (USPTO) on April 28, 2004, is not included in the issued patent. A Form PTO/SB/44 is attached, which directs replacement of the entire sequence listing of the issued patent with the substitute sequence listing filed on April 28, 2004. The proposed corrections do not constitute new matter or require reexamination.

The official action mailed January 16, 2004, included a third notice to comply with sequence listing requirements. In response to the notice to comply, a substitute sequence listing was filed April 28, 2004, along with an amendment to employ sequence modifiers consistent with the substitute sequence listing. The amendments to the specification appear in the issued patent, however, the substitute sequence listing is omitted. A copy of the complete submission of April 28, 2004, is enclosed, including a date-stamped cover sheet indicating receipt by the USPTO. Essentially,

JUN 14 2005

the Patent Office, in error, printed the above-reference patent with an incorrect, prior version of the specification.

Based on the foregoing, applicants believe that issuance of the patent with an incorrect sequence listing is the result of error on the part of the USPTO. Although the applicant believes no fee is due for processing of this request, should the Patent Office determine otherwise, such fees (for the processing of this request) may be charged to Deposit Account No. 33975 under Order No. 037003-027540.

Respectfully submitted,

PILLSBURY WINTHROP SHAW PITTMAN LLP

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Registration No. 40,944

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McLean, VA 22102  
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Date: June 9, 2005

TAC/JBM

UNITED STATES PATENT AND TRADEMARK OFFICE  
CERTIFICATE OF CORRECTION

PATENT NO : 6893636

DATED : May 17, 2005

INVENTOR(S) :

MITCHELL E REFF, ET AL

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In Sequence Listing,  
replace "Sequence Listing"  
with --attached Sequence Listing--.

MAILING ADDRESS OF SENDER:

PILLSBURY WINTHROP SHAW PITTMAN LLP  
P.O. Box 10500  
McLean, VA 22102

PATENT NO. 6893636

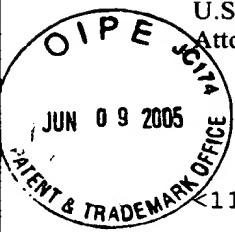
No. of additional copies



This collection of information is required by 37 CFR 1.322, 1.323, and 1.324. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 1.0 hour to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Attention Certificate of Corrections Branch, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

*If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.*

JUN 14 2005



U.S. Application No. 09/019,441  
Attorney Ref. No. 037003-0275470

SEQUENCE LISTING

<110> REFF, MITCHELL E.  
KLOETZER, WILLIAM S.  
NAKAMURA, TAKEHIKO

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS

<130> 037003-0275470

<140> 09/019,441  
<141> 1998-02-05

<150> 08/803,085  
<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

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<222> (1)..(57)

<223> leader sequence

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<222> (58)..(390)

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<221> CDS

<222> (1)..(390)

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-15 -10 -5

tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct 96  
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt 144  
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc	192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	
ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct	240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	
gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile	
65 70 75	
tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat	336
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr	
80 85 90	
aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc	384
Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val	
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Leu Gly	
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<210> 2  
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<212> PRT  
<213> Artificial Sequence

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-15 -10 -5

Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala  
30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser  
50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile  
65 70 75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr  
80 85 90

Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val  
95 100 105

Leu Gly  
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<210> 3  
<211> 423  
<212> DNA  
<213> Artifical Sequence

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<220>  
<221> misc\_feature  
<222> (1)..(57)  
<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(423)

<220>  
<221> CDS  
<222> (1)..(423)

<400> 3

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															-5		
																-15	

gtc	ctg	tcc	cag	ctg	cag	ctg	cag	gag	tcg	ggc	cca	gga	gtg	gtg	aag	96	
Val	Leu	Ser	Gln	Leu	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Val	Val	Lys		
																-1	
																5	

cct	tcg	gag	acc	ctg	tcc	ctc	acc	tgc	gct	gtc	tct	ggt	ggc	tct	gtc	144	
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Val		
																15	
																20	

agc	agt	agt	aac	tgg	tgg	acc	tgg	atc	cgc	cag	ccc	cca	ggg	aag	gga	192	
Ser	Ser	Ser	Asn	Trp	Trp	Thr	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly		
																30	
																35	

ctg	gag	tgg	att	gga	cgt	atc	tct	ggt	agt	ggt	ggg	gcc	acc	aac	tac	240	
Leu	Glu	Trp	Ile	Gly	Arg	Ile	Ser	Gly	Ser	Gly	Gly	Ala	Thr	Asn	Tyr		
																50	
																55	

aac	ccg	tcc	ctc	aag	agt	cga	gtc	atc	att	tca	caa	gac	acg	tcc	aag	288	
Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Ile	Ile	Ser	Gln	Asp	Thr	Ser	Lys		
																65	
																70	

aac	cag	ttc	tcc	ctg	aac	ctg	aac	tct	gtg	acc	gcc	gcg	gac	acg	gcc	336	
Asn	Gln	Phe	Ser	Leu	Asn	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala		
																80	
																85	

gtg	tat	tac	tgt	gcc	aga	gat	tgg	gcc	caa	ata	gct	gga	aca	acg	cta	384	
Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Trp	Ala	Gln	Ile	Ala	Gly	Thr	Thr	Leu		
																95	
																100	

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca  
Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

423

<210> 4  
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<212> PRT  
<213> Artifical Sequence

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<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 4

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Ala Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 5  
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<212> DNA  
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atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg	48			
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-20	-15	-10		
ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc	96			
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser				
-5	-1	1	5	10
ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt	144			
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser				
15	20	25		
cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa	192			
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys				
30	35	40		
gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc	240			
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val				
45	50	55		
cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc	288			
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr				
60	65	70		
gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag	336			
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln				
75	80	85	90	
gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc	384			
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile				
95	100	105		
aaa	387			
Lys				

<210> 6  
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<212> PRT  
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<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 6

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp		
-20	-15	-10
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser		



acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag	192
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln	
30 35 40 45	
ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg	240
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp	
50 55 60	
tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc	288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala	
65 70 75	
aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg	336
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90	
gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc	384
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly	
95 100 105	
cag gga gtc ctg gtc acc gtc tcc tca	411
Gln Gly Val Leu Val Thr Val Ser Ser	
110 115	

<210> 8  
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Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys	
-1 1 5 10	
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe	
15 20 25	
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln	
30 35 40 45	
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp	
50 55 60	
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala	
65 70 75	
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90	
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly	
95 100 105	

Gln Gly Val Leu Val Thr Val Ser Ser  
110 115

<210> 9  
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<400> 9  
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<210> 10  
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<400> 10  
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<400> 12  
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<212> DNA  
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<400> 13

ggtgtcagcca ccgttagcttt gatytccasc tt

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<210> 14  
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<210> 29

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

<400> 31

ccaggccact gtcacggctt c

21

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<212> DNA

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Attorney Ref. No. 037003-0275470

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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cagagctggg tacgtcctca

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<210> 34

<211> 20

<212> DNA

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<210> 35

<211> 20

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<212> DNA

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<400> 36

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<210> 39  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 39

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27

SEQUENCE LISTING

<110> REFF, MITCHELL E.  
KLOETZER, WILLIAM S.  
NAKAMURA, TAKEHIKO

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE  
THEREOF AS THERAPEUTICS

<130> 037003-0275470

<140> 09/019,441  
<141> 1998-02-05

<150> 08/803,085  
<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

<210> 1  
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<223> Description of Artificial Sequence: Mature peptide is derived from Old  
World Monkey (macaque); leader sequence is an artificial sequence to  
facilitate cloning

<220>  
<221> misc\_feature  
<222> (1)..(57)  
<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(390)

<220>  
<221> CDS  
<222> (1)..(390)

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atg gcc tgg act ctg ctc ctc gtc acc ctc ctc act cag ggc aca gga 48  
Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly  
-15 -10 -5

tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct 96  
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt 144  
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc	192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	
ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct	240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	
gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile	
65 70 75	
tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat	336
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr	
80 85 90	
aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc	384
Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val	
95 100 105	
cta ggt	390
Leu Gly	
110	

<210> 2  
<211> 130  
<212> PRT  
<213> Artifical Sequence

<220>

<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 2

Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly	
-15 -10 -5	
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser	
-1 1 5 10	
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val	
15 20 25	
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile	
65 70 75	
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr	
80 85 90	
Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val	
95 100 105	

Leu Gly  
110

<210> 3  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(423)

<220>  
<221> CDS  
<222> (1)..(423)

<400> 3

atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga gtg gtg aag 96  
Val Leu Ser Gln Leu Gln Leu Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

cct tcg gag acc ctg tcc acc tgc gct gtc tct ggt ggc tct gtc 144  
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga 192  
Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac 240  
Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Ala Thr Asn Tyr  
50 55 60

aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag 288  
Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc 336  
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta 384  
Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca  
Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

423

<210> 4  
<211> 141  
<212> PRT  
<213> Artifical Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old  
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facilitate cloning

<400> 4

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 5  
<211> 387  
<212> DNA  
<213> Artifical Sequence

<220>  
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facilitate cloning

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<223> leader sequence

<220>

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<222> (67)..(387)

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<400> 5

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg 48  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
-20 -15 -10

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96  
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
-5 -1 1 5 10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144  
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
15 20 25

cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192  
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
30 35 40

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240  
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val  
45 50 55

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
60 65 70

gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336  
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
75 80 85 90

gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc 384  
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
95 100 105

aaa 387  
Lys

<210> 6  
<211> 129  
<212> PRT  
<213> Artifical Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old  
World Monkey (macaque); leader sequence is an artificial sequence to  
facilitate cloning

<400> 6

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
-20 -15 -10

Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

-5                    -1            1                    5                    10

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
15                    20                                    25

Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
30                    35                                    40

Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val  
45                    50                                    55

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
60                    65                                    70

Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
75                    80                                    85                    90

Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
95                    100                                    105

Lys

<210> 7  
<211> 411  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<220>  
<221> misc\_feature  
<222> (1)..(57)  
<223> leader sequence

<220>  
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<222> (58)..(411)

<220>  
<221> CDS  
<222> (1)..(411)

<400> 7

atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt cct ctt ttg aaa ggt      48  
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15                    -10                            -5

gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag      96  
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys  
-1                    5                                    10

cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc      144  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe  
15                    20                                    25

acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag	192
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln	
30 35 40 45	
ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg	240
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp	
50 55 60	
tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc	288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala	
65 70 75	
aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg	336
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90	
gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc	384
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly	
95 100 105	
cag gga gtc ctg gtc acc gtc tcc tca	411
Gln Gly Val Leu Val Thr Val Ser Ser	
110 115	

<210> 8  
<211> 137  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 8

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys  
-1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe  
15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln  
30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp  
50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala  
65 70 75

Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
80 85 90

Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly  
95 100 105

Gln Gly Val Leu Val Thr Val Ser Ser  
110 115

<210> 9  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 9  
atcacagatc tctcaccatg gacatgaggg tcccccgtca g 41

<210> 10  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 10  
atcacagatc tctcaccatg aggctccctg ctcag 35

<210> 11  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
atcacagatc tctcaccatg gaarccccag ckca 35

<210> 12  
<211> 38  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
atcacagatc tctcaccatg gtgttgca cccagg 38

<210> 13  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 13

ggtgtcagcca ccgttagcttt gatytccasc tt

32

<210> 14  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14

atcacagatc tctcaccatg rcctgstccc ctct

34

<210> 15  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15

atcacagatc tctcaccatg gcctggrrtc ygct

34

<210> 16  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16

atcacagatc tctcaccatg gcmtggaycc ctctc

35

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17

cttgggctga cctaggacgg t

21

<210> 18  
<211> 30

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18

gcgactaagt cgaccatgga ctggacacctgg

30

<210> 19  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19

gcgactaagt cgaccatgaa acacacctgtgg

30

<210> 20  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20

gcgactaagt cgaccatgga gtttgggctg agc

33

<210> 21  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21

gcgactaagt cgaccatggg gtcaaccgcc atc

33

<210> 22  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 22

gcgactaagt cgaccatgtc tgtctccttc ctc

33

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<210> 23  
<211> 46  
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<220>  
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<400> 23

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46

<210> 24  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 24

gatggggccct tggtgcttagc tgaggagacg g

31

<210> 25  
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<212> DNA  
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<400> 25

ggtgcttagct gaggagacgg tgaccaggac tccctggccc cagaaggcta g

51

<210> 26  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
<400> 26

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17

<210> 27  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27

gttttcccag tcacga

16

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28

atatacgact cactataggg

20

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

ccgtcagatc gcctggagac gcca

24

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gcagttccag atttcaactg

20

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ccaggccact gtcacggctt c

21

<210> 32

<211> 20

<212> DNA

U.S. Application No. 09/019,441  
Attorney Ref. No. 037003-0275470

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

cagagctggg tacgtcctca

20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

ccccccagag gtgctcttgg

20

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

acacagaccc gtcgacatgg

20

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

gctctcgag gtgctcctgg

20

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

acagacccgt cgaccatgga gtttggctg

30

<210> 37  
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<400> 37

cccccgtggc ctagctgagg agacggt

27

<210> 38  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 38

agagagaacg ccaagaacac actgttt

27

<210> 39  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 39

aaacagtgtg ttcttggcgt tctctct

27

**COPY**

JUN 09 2005



**RECEIPT FROM PTO FOR INDICATED ITEMS**

(Do NOT Use for New or Continuing Applications of Any Kind)  
Use 2 postcards for all New Applns. (cont/Div/CIP, too)  
Use this sheet when filing CPA

Appn. No: 09/019,441	Atty: Thomas A. Cawley, Jr./JBM/NTBerg
First Inventor: REFF	Date: April 28, 2004
	Matter No: 0275470
	Client No: 037003

**ENCLOSED:**

- Amendment
- Copy of Notice to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequences
- Substitute Sequence Listing (Paper Copy and CRF Copy)
- Statement Pursuant to 37 C.F.R. 1.821(f)
- Petition for One-Month Extension of Time

**\$110.00** Amount Requested be Charged to our Dep. Acct. No. 03-3975

**Current DUE DATE:**

**May 16, 2004**

(Submit Single Copy Only)





## RECEIPT FROM PTO FOR INDICATED ITEMS

(Do NOT Use for New or Continuing Applications of Any Kind)  
Use 2 postcards for all New Applns. (cont/Div/CIP, too)  
Use this sheet when filing CPA

Appln. No: 09/019,441	Atty: Thomas A. Cawley, Jr./JBM/NTBerg
First Inventor: REFF	Date: April 28, 2004
	Matter No: 0275470
	Client No: 037003

### ENCLOSED:

- Amendment
- Copy of Notice to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequences
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- Statement Pursuant to 37 C.F.R. 1.821(f)
- Petition for One-Month Extension of Time

**\$110.00** Amount Requested be Charged to our Dep. Acct. No. 03-3975

Current DUE DATE:

May 16, 2004

(Submit Single Copy Only)

U.S. Patent Appl. No. 09/019,441  
Attorney Docket No. 037003-0275470



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re PATENT APPLICATION OF

Mitchell R. REFF et al.

Group Art Unit: 1644

Application Serial No. 09/019,441

Examiner: Phuong N. Huynh

Filed: February 5, 1998

Title: GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES  
AND USE THEREOF AS THERAPEUTICS

\* \* \* \* \*

**AMENDMENT PURSUANT TO 37 C.F.R. § 1.111**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

This is in response to the official action dated January 16, 2004, wherein the claims were rejected under 35 U.S.C. § 112, second paragraph. The applicants traverse the outstanding rejections in view of the following amendments and remarks. This response is timely filed with the enclosed petition for a one-month extension of time and payment of the requisite fee.

**Amendments To The Specification**

Please amend the paragraph beginning at page 43, line 23, as follows:

A second independent PCR amplification of the light chain from cDNA of primate monoclonal antibody 6G5 was effected using a 5' primer early leader sequence of lambda light chain family 2 (primer 745) (SEQ ID NO: 15) and the 3' J region primer 926 (SEQ ID NO: 17). (See Primers for PCR of the lambda light chain variable domain of 6G5 in Tables 1-3 (SEQ ID NOs: 9-25). The isolated PCR product (see technique above) was cloned into TA vector by using the Original TA Cloning( Kit (Invitrogen Catalog # K2000-01). The isolated miniprep DNA (see technique above) was examined under agarose gel electrophoresis after digestion with EcoR I restriction endonuclease. The resultant PCR product comprised in the TA vector was then sequenced (as described previously) using Sp6 (SEQ ID NO: 26) and M13(-40) (SEQ ID NO: 27) forward primers (See Sequencing primers in Table 4 (SEQ ID NOs: 26-35)). The resultant light chain sequence was identical to that of light chain from the first PCR. This entire sequence of the light chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 is presented below (SEQ ID NO: 1) as an alignment of the nucleotide sequence (SEQ ID NO:1) and the encoded amino acid sequence (SEQ ID NO:2).

Please amend the captioned section beginning at page 44, line 8, as follows:

**Light chain variable region of primate monoclonal antibody**  
**anti-human CD23 6G5 Leader**

Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr  
ATG GCC TGG ACT CTG CTC CTC GTC ACC CTC CTC ACT CAG GGC ACA  
-1

Gly Ser Trp Ala

GGA TCC TGG GCT (SEQ ID NO: 1 – bases 1-57)

Please amend the captioned section beginning at page 44, line 15, as follows:

**Mature Protein (Numbering is Kabat)**

**Framework 1**

1	9	11
Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly		
CAG TCT GCC CCG ACT CAG CCT CCC TCT GTG TCT GGG TCT CCT GGA		

20 23

Gln Ser Val Thr Ile Ser Cys

CAG TCG GTC ACC ATC TCC TGC (SEQ ID NO: 1 – bases 58-123)

Please amend the captioned section beginning at page 44, line 23, as follows:

**CDR1**

24 27 27A 27B 27C 28 34

Thr Gly Thr Ser Asp Asp Val Gly Gly Tyr Asn Tyr Val Ser  
ACT GGA ACC AGC GAT GAC GTT GGT TAT AAC TAT GTC TCC  
(SEQ ID NO: 1 – bases 124-165)

Please amend the captioned section beginning at page 44, line 27, as follows:

**Framework 2**

35 40 49

Trp Tyr Gln His His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr  
TGG TAC CAA CAC CAC CCA GGC AAA GCC CCC AAA CTC ATG ATT TAT  
(SEQ ID NO: 1 – bases 166-210)

Please amend the captioned section beginning at page 45, line 1, as follows:

**CDR2**

50 56

Asp Val Ala Lys Arg Ala Ser

GAT GTC GCT AAG CGG GCC TCA (SEQ ID NO: 1 – bases 211-231)

Please amend the captioned section beginning at page 45, line 5, as follows:

**Framework 3**

57 60 70

Gly Val Ser Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala  
GGG GTC TCT GAT CGC TTC TCT GGC TCC AAG TCT GGC AAC ACG GCC  
80

Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr  
TCC CTG ACC ATC TCT GGG CTC CAG GCT GAG GAC GAG GCT GAT TAT

88

Tyr Cys

TAC TGT (SEQ ID NO: 1 – bases 232-327)

Please amend the captioned section beginning at page 45, line 15, as follows:

**CDR 3**

89	90	95	95A	96	97				
Cys	Ser	Tyr	Thr	Thr	Ser	Ser	Thr	Leu	Leu
TGT	TCA	TAT	ACA	ACC	AGT	AGC	ACT	TTG	TTA

(SEQ ID NO: 1 – bases 328-357)

Please amend the captioned section beginning at page 45, line 19, as follows:

**Framework 4**

98	100	106	106A	107						
Phe	Gly	Arg	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly
TTC	GGA	AGA	GGG	ACC	CGG	TTG	ACC	GTC	CTA	GGT

(SEQ ID NO: 1 – bases 358-390)

Please amend the captioned section beginning at page 45, line 23, as follows:

**2) Cloning the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 by PCR**

The first PCR amplification of the heavy chain variable domain from cDNA of primate monoclonal antibody 6G5 was performed by using the set of early leader sequence primers described supra and the 3' J region primer GE244 (SEQ ID NO: 23). These primers are in Tables 1-3 (SEQ ID NOs: 9-25) infra. This reaction resulted in a 350 base PCR product. This 350 base product (purified as described supra), was digested with Nhe I and Sal I, and ligated into N5LG1 and digested with the same endonucleases in the first PCR amplification. The resultant ligation mixture was transformed into host cells using the same techniques for cloning the light chain. Plasmid N5LG1 containing the 350 base PCR product was then isolated and sequenced (using sequencing primers 266 (SEQ ID NO: 32) and 268) (SEQ ID NO: 33). (These Sequencing primers are set forth in Table 4 (SEQ ID NOs: 26-35).)

Please amend the paragraph beginning at page 46, line 15, as follows:

A second independent PCR reaction was conducted to amplify and isolate the heavy chain variable domain of primate monoclonal antibody 6G5 using a 5' early leader sequence primer for family 1 (MB1503) (SEQ ID NO: 18) and a 3' J' region primer GE244 (SEQ ID NO: 23). (These primers are also contained in Tables 1-3 (SEQ ID NOs: 9-25)) The resultant

PCR product was then cloned into the NSLG1 using the same techniques described supra. Its sequence was found to be identical to the first PCR product.

Please amend the paragraph beginning at page 46, line 24, as follows:

Therefore, in order to clone the whole heavy variable domain of 6G5 including the missing 5' terminus a new longer 3' primer (MB1533) (SEQ ID NO: 25) which included the CDR3 and framework 4 regions of the 6G5 heavy variable chain was then used in a third independent PCR reaction with the family 1 5' primer (MB1503) (SEQ ID NO: 18). (These primers are also contained in Tables 1-3 (SEQ ID NOs: 9-25).

Please amend the captioned section beginning at page 47, line 6, as follows:

A fourth independent PCR was performed using the same primers as the third PCR amplification. This resulted in a PCR product which was isolated and cloned into the TA vector as described previously. The sequence of the fourth independent PCR product was found to be identical to that obtained in the third PCR amplification. This sequence, which comprises the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5, is presented below (~~SEQ ID NO: 2~~) as an alignment of the nucleotide sequence (SEQ ID NO: 3) and the encoded amino acid sequence (SEQ ID NO:4).

Please amend the captioned section beginning at page 47, line 15, as follows:

**Heavy chain variable region of primate monoclonal antibody anti-human CD23 6G5**  
**Leader**

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg  
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA

-1

Trp Val Leu Ser

TGG GTC CTG TCC (SEQ ID NO: 3 – bases 1-57) -

Please amend the captioned section beginning at page 47, line 23, as follows:

**Mature Protein (Numbering is Kabat)**  
**Framework 1**

1

10

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys Pro Ser  
CAG CTG CAG CTG CAG GAG TCG GGC CCA GGA GTG GTG AAG CCT TCG

20

30

Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val Ser  
GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCT GTC AGC  
(SEQ ID NO: 3 – bases 58-147)

Please amend the captioned section beginning at page 48, line 1, as follows:

**CDR 1**

31

35 35a

Ser Ser Asn Trp Trp Thr

AGT AGT AAC TGG TGG ACC (SEQ ID NO: 3 – bases 148-165)

Please amend the captioned section beginning at page 48, line 5, as follows:

**Framework 2**

36

40

49

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly  
TGG ATC CGC CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT GGA  
(SEQ ID NO: 3 – bases 166-207)

Please amend the captioned section beginning at page 48, line 16, as follows:

**CDR2**

50

52 52A 53

60

Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr Asn Pro Ser Leu  
CGT ATC TCT GGT AGT GGT GGG GCC ACC AAC TAC AAC CCG TCC CTC  
65

Lys Ser

AAG AGT (SEQ ID NO: 3 – bases 208-258)

Please amend the captioned section beginning at page 48, line 16, as follows:

**Framework 3**

66

70

80

Arg Val Ile Ile Ser Gln Asp Thr Ser Lys Asn Gln Phe Ser Leu  
CGA GTC ATC ATT TCA CAA GAC ACG TCC AAG AAC CAG TTC TCC CTG

82 82a 82b 82c 83 90  
Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
AAC CTG AAC TCT GTG ACC GCC GCG GAC ACG GCC GTG TAT TAC TGT  
94  
Ala Arg  
GCC AGA (SEQ ID NO: 3 – bases 259-354)

Please amend the captioned section beginning at page 48, line 26, as follows:

**CDR 3**

95 100 100a 100b 100c 100d 101 102  
Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu Gly Phe  
GAT TGG GCC CAA ATA GCT GGA ACA ACG CTA GGC TTC  
(SEQ ID NO: 3 – bases 355-390)

Please amend the captioned section beginning at page 49, line 1, as follows:

**Framework 4**

103 110 113  
Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA (SEQ ID NO: 3 – bases 391-423)

Please amend the captioned section beginning at page 50, line 3, as follows:

**1. Cloning the light chain variable domain of primate monoclonal anti-human CD23 antibody 5E8 by PCR**

The first PCR reaction of the light chain variable domain from FEE cDNA was carried out using a set of kappa early leader sequence primers and the 3' J region primer GE204 (SEQ ID NO: 13). (See primers for PCR of the kappa light chain variable domain of 5E8 in Tables 1-3 (SEQ ID NOs: 9-25)). A 420 base PCR product was obtained. The isolated 420 base PCR product was digested with Bgl II and BsiW I restriction endonucleases, cloned into the mammalian expression vector N5KG4P and sequenced using GE108 (SEQ ID NO: 29) and 377 (SEQ ID NO: 30) primers (which are contained in Table 4 (SEQ ID NOs: 26-35)): The mammalian expression vector N5KG4P is identical to the vector N5LG4P except it contains the human kappa light chain constant region in place of the human lambda light

Please amend the captioned section beginning at page 51, line 17, as follows:

**CDR 1**

24

30

34

Arg Ala Ser Gln Asp Ile Arg Tyr Tyr Leu Asn

AGG GCA AGT CAG GAC ATT AGG TAT TAT TTA AAT (SEQ ID NO: 5 – bases 136-168)

Please amend the captioned section beginning at page 51, line 21, as follows:

**Framework 2**

35

40

49

Try Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC TAT

(SEQ ID NO: 5 – bases 169-213)

Please amend the captioned section beginning at page 51, line 25, as follows:

**CDR2**

50

56

Val Ala Ser Ser Leu Gln Ser

GTT GCA TCC AGT TTG CAA AGT (SEQ ID NO: 5 – bases 214-234)

Please amend the captioned section beginning at page 51, line 29, as follows:

**Framework 3**

57

60

70

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe  
GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAG TTC

80

Thr Leu Thr Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr  
ACT CTC ACC GTC AGC AGC CTG CAG CCT GAA GAT TTT GCG ACT TAT

88

Tyr Cys

TAC TGT (SEQ ID NO: 5 – bases 235-330)

Please amend the captioned section beginning at page 52, line 7, as follows:

**CDR 3**

89 90

97

Leu Gln Val Tyr Ser Thr Pro Arg Thr

CTA CAG GTT TAT AGT ACC CCT CGG ACG (SEQ ID NO: 5 – bases 331-357)

Please amend the captioned section beginning at page 52, line 11, as follows:

**Framework 4**

98 100

107

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA (SEQ ID NO: 5 – bases 358-387)

Please amend the captioned section beginning at page 52, line 15, as follows:

**2) Cloning the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 5E8 by PCR**

The first PCR of the heavy chain variable domain of 5E8 was performed using a set of 5' early leader heavy chain sequence primers and the 3' primer GE210 (SEQ ID NO: 24). (See primers for PCR of the heavy chain variable domain of 6G5 and 5E8 in Table 1 (SEQ ID NOs: 9-13)). A 420 base PCR product appeared in the family 3 primer reaction. The PCR product was purified and then digested with Nhe I and Sal I and cloned into the mammalian expression vector N5KG4P vector (as described previously). The PCR product was sequenced using the 268 (SEQ ID NO: 33) and 928 (SEQ ID NO: 35) primers. (See sequencing primers in Table 4 (SEQ ID NOs: 26-35)).

Please amend the paragraph beginning at page 52, line 28, as follows:

A second independent PCR of the heavy chain variable domain of 5E8 was performed using the family 3 5' primer GE207 (SEQ ID NO: 20) and the 3' primer GE210 (SEQ ID NO: 24). (See primers for PCR of the, heavy chain variable domain of 6G5 and 5E8 in Tables 1-3 (SEQ ID NOs: 9-25)). The isolated PCR product was cloned into a TA vector using the same techniques previously described and sequenced by using Sp6 (SEQ ID NO: 26) and T7 (SEQ ID NO: 28) primers. Sequencing revealed that the TAC at codon 91 had been changed into TGC.

Please amend the paragraph beginning at page 53, line 6, as follows:

In order to determine the appropriate codon at 91, a third independent PCR was performed using the same primers as the second PCR (see above). The PCR product was again cloned into a TA vector and sequenced using Sp6 (SEQ ID NO: 26) and T7 (SEQ ID NO: 28) primers. The sequence was found to be identical to the heavy chain variable sequence obtained in the first PCR. Therefore, the TGC at position 91 in the second independent PCR product is apparently the result of an error introduced during PCR. This entire sequence of the heavy chain variable domain of primate monoclonal anti-human CD23 antibody 6G5 is presented below (SEQ ID NO: 4), as an alignment of the nucleotide sequence (SEQ ID NO: 7) and the encoded amino acid sequence (SEQ ID NO: 8).

Please amend the captioned section beginning at page 53, line 18, as follows:

**Heavy chain variable region of primate monoclonal antibody**  
**anti-human CD23 5E8 Leader**

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys  
ATG GAG TTT GGG CTG AGC TGG GTT TTC CTT GTT CCT CTT TTG AAA  
-1  
Gly Val Gln Cys  
GGT GTC CAG TGT (SEQ ID NO: 7 - bases 1-57)

Please amend the captioned section beginning at page 53, line 26, as follows:

**Mature Protein (Numbering is Kabat)**

**Framework 1**

1	10
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys Pro Gly	
GAG GTG CAG CTG GTG GAG TCT GGG GGC GGC TTG GCA AAG CCT GGG	
20	30
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe Thr	
GGG TCC CTG AGA CTC TCC TGC GCA GCC TCC GGG TTC AGG TTC ACC	
( <u>SEQ ID NO: 7 - bases 58-147</u> )	

Please amend the captioned section beginning at page 54, line 2, as follows:

**CDR 1**

31 35 35a 35b  
Phe Asn Asn Tyr Tyr Met Asp  
TTC AAT AAC TAC TAC ATG GAC (SEQ ID NO: 7 - bases 148-168)

Please amend the captioned section beginning at page 54, line 6, as follows:

## **Framework 2**

36 40 49  
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Ser  
TGG GTC CGC CAC GCA CCA GGG CAG GGG CTG GAG TGG GTC TCA  
(SEQ ID NO: 7 - bases 169-210)

Please amend the captioned section beginning at page 54, line 10, as follows:

## CDR2

50 52 52A 53 60  
Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp Tyr Ala Asp Ser Val  
CGT ATT AGT AGT AGT GGT GAT CCC ACA TGG TAC GCA GAC TCC GTG  
65  
Lys Gly  
AAG GGC (SEQ ID NO: 7 - bases 211-261)

Please amend the captioned section beginning at page 54, line 17, as follows:

### Framework 3

66	70	80
Arg Phe Thr Ile Ser Arg Glu Asn Ala Asn Asn Thr Leu Phe Leu		
AGA TTC ACC ATC TCC AGA GAG AAC GCC AAC AAC ACA CTG TTT CTT		
82	82a	82b
82c	83	90
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTC TAT TAC TGT		
94		
Ala Ser		
GCG AGC (SEQ ID NO: 7 - bases 262-357 )		

Please amend the captioned section beginning at page 54, line 27, as follows:

**CDR 3**

95                    100 101  
Leu Thr Thr Gly Ser Asp Ser  
TTG ACT ACA GGG TCT GAC TCC (SEQ ID NO: 7- bases 358-378)

Please amend the captioned section beginning at page 55, line 1, as follows:

**Framework 4**

103                    110                    113  
Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA (SEQ ID NO: 7 - bases 379-411)

Please amend the paragraph beginning at page 56, line 3, as follows:

A first PCR was done using NSKG4P + 5E8 as a template and a 3' primer (corresponding to codon 71 to 79) and which contains a mutation at codon 75 (AAC changed to AAG, Primer MB1654 (SEQ ID NO: 39), and a 5' primer at the beginning of the leader sequence (Primer MB1650) (SEQ ID NO: 36). (See PCR Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region 5E8 set forth in Table 5 (SEQ ID NOs: 36-39)).

Please amend the paragraph beginning at page 56, line 11, as follows:

A second PCR was performed on the same template by using a 5' primer (corresponding to codon 71 to 79) containing the same mutation (Primer MB1653) (SEQ ID NO: 38) and a 3' primer from the end of framework 4 (Primer MB1651) (SEQ ID NO: 37) (See PCR Primers Used for the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region of 5E8 in Table 5 (SEQ ID NOs: 36-39).)

Please amend the paragraph beginning at page 56, line 18, as follows:

These two PCR products were isolated and mixed in equal molar ratios. A third independent PCR was then carried out by using the mixture of the first and second PCP products as a template with a 5' primer used in the first PCR (MB1650) (SEQ ID NO: 36) and a 3' primer used in the second PCR (MP 1651) (SEQ ID NO: 37) (See PCP Primers Used for

the Generation of a Glycosylation Mutant of the Heavy Chain Variable Region in Table 5 (SEQ ID NOs: 36-39.) The PCR product obtained in third PCR was found to contain the heavy variable domain coding region of 5E8 wherein the asparagine 75 had been changed to lysine.

Please amend Tables 1-5 beginning at page 57, line 8 (in their entirety), as follows:

Table 1

Primers for PCR of the kappa light chain variable domain of 5E8

NAME	<u>Light chain V<sub>k</sub> -early leader 5' (Bgl II)</u>	FAMILY
	-22 -21 -20 -19 -18 17 -16 -15 -14	
GE201 5' AT CAC <u>AGA TCT</u> CTC ACC ATG GAC ATG AGG GTC CCC GCT	CAG 3'	1
{SEQ ID NO: 5} <u>(SEQ ID NO: 9)</u>		
GE200 5' AT CAC <u>AGA TCT</u> CTC ACC	ATG AGG CTC	CCT GCT
{SEQ ID NO: 6} <u>(SEQ ID NO: 10)</u>		CAG 3'
GE202 5' AT CAC <u>AGA TCT</u> CTC ACC	ATG GAA (A/G)CC CCA GC(T/G)	CAG 3'
{SEQ ID NO: 7} <u>(SEQ ID NO: 11)</u>		3
GE203 5' AT CAC <u>AGA TCT</u> CTC ACC	ATG GTG TTG	CAG ACC CAG GTC 3'
{SEQ ID NO: 8} <u>(SEQ ID NO: 12)</u>		4

Light chain V<sub>k</sub>-3' primer (BsiW I)

113 112 111 110 109 108 107 106 105 104 103  
GE204 5' GG TGC AGC CAC CGT AGC TTT GAT (C/T)TC CA(G/C) CTT 3'  
{SEQ ID NO: 9} (SEQ ID NO: 13)

Table 2

Primers for PCR of the lambda light chain variable domain of 6G5

NAME	<u>Light chain V<sub>l</sub> -early leader 5' (Bgl II)</u>	FAMILY
	-20 -19 -18 -17 -16 -15	
744 5' AT CAC <u>AGA TCT</u> CTC ACC ATG (G/A)CC TG(G/C) TCC	CCT CT 3'	1
{SEQ ID NO: 10} <u>(SEQ ID NO: 14)</u>		
745 5' AT CAC <u>AGA TCT</u> CTC ACC ATG GCC	TGG (A/G)CT C(T/C)G CT 3'	2

~~(SEQ ID NO: 11)~~ (SEQ ID NO: 15)

910 5' AT CAC AGA TCT CTC ACC ATG GC(A/C) TGG A(T/C)C CCT CTC 3' 3

~~(SEQ ID NO: 12)~~ (SEQ ID NO: 16)

Light chain V1-3' primer (Avr II)

110 109 108 107 106 105 104

926 5' (AC)10 CTT GGG CTG ACC TAG GAC GGT 3' ~~(SEQ ID NO: 13)~~ (SEQ ID NO: 17)

**Table 3**

**Primers for PCR of the heavy chain  
variable domains from 6G5 and 5E8**

NAME	<u>Heavy chain-early leaders 5' (Sal I)</u>	<u>Family</u>
	-20 -19 -18 -17 -16 -15	
MB1503 5' GCG ACT AAG <u>TCG ACC</u> ATG GAC TGG ACC TGG	3'	1
<del>(SEQ ID NO: 14)</del> <u>(SEQ ID NO: 18)</u>		
MB1502 5' GCG ACT AAG <u>TCG ACC</u> ATG AAA CAC CTG TGG	3'	2, 4
<del>(SEQ ID NO: 15)</del> <u>(SEQ ID NO: 19)</u>		
GE207 5' GCG ACT AAG <u>TCG ACC</u> ATG GAG TTT GGG CTG AGC 3'		3
<del>(SEQ ID NO: 16)</del> <u>(SEQ ID NO: 20)</u>		
GE208 5' GCG ACT AAG <u>TCG ACC</u> ATG GGG TCA ACC GCC ATC 3'		5
<del>(SEQ ID NO: 17)</del> <u>(SEQ ID NO: 21)</u>		
GE209 5' GCG ACT AAG <u>TCG ACC</u> ATG TCT GTC TCC TTC CTC 3'		6
<del>(SEQ ID NO: 18)</del> <u>(SEQ ID NO: 22)</u>		

Heavy chain-3' primer (Nhe I)

120 119 118 117 116 115 114 113 112 111 110

GE244 5' GC CAG GGG GAA GAC CGA TGG GCC CTT GGT GCT AGC TGA GGA GAC GG 3'  
~~(SEQ ID NO: 19)~~ (SEQ ID NO: 23)

GE210 5' GA TGG GCC CTT GGT GCT AGC TGA GGA GAC GG 3'  
~~(SEQ ID NO: 20)~~ (SEQ ID NO: 24)

MB1533 5' GGT GCT AGC TGA GGA GAC GGT  
109 108 107 106 105 104 103 101 100 99  
GAC CAG GAC TCC CTG GCC CCA GAA GCC TAG 3'  
~~(SEQ ID NO: 21)~~ (SEQ ID NO: 25)

**Table 4**  
**Sequencing Primers**

Sp6 primer <u>NO: 26)</u>	5' AT TTA GGT GAC ACT ATA	3' <del>(SEQ ID NO: 22)</del> <u>(SEQ ID</u>
M13 (-40) Forward Primer <u>NO: 27)</u>	5' GTT TTC CCA GTC ACG A	3' <del>(SEQ ID NO: 23)</del> <u>(SEQ ID</u>
T7 Promoter Primer <u>ID NO: 28)</u>	5' AT ATA CGA CTC ACT ATA GGG	3' <del>(SEQ ID NO: 24)</del> <u>(SEQ</u>
GE 108 Primer <u>(SEQ ID NO: 29)</u>	5' CCG TCA GAT CGC CTG GAG ACG CCA	3' <del>(SEQ ID NO: 25)</del>
377 Primer <u>ID NO: 30)</u>	5' GCA GTT CCA GAT TTC AAC TG	3' <del>(SEQ ID NO: 26)</del> <u>(SEQ</u>
607 PRIMER <u>ID NO: 31)</u>	5' CCA GGC CAC TGT CAC GGC TTC	3' <del>(SEQ ID NO: 27)</del> <u>(SEQ</u>
266 PRIMER <u>ID NO: 32)</u>	5' CAG AGC TGG GTA CGT CCT CA	3' <del>(SEQ ID NO: 28)</del> <u>(SEQ</u>
268 PRIMER <u>ID NO: 33)</u>	5' GCC CCC AGA GGT GCT CTT GG	3' <del>(SEQ ID NO: 29)</del> <u>(SEQ</u>
876 PRIMER <u>ID NO: 34)</u>	5' ACA CAG ACC CGT CGA CAT GG	3' <del>(SEQ ID NO: 30)</del> <u>(SEQ</u>
928 PRIMER <u>ID NO: 35)</u>	5' GCT CTC GGA GGT GCT CCT GG	3' <del>(SEQ ID NO: 31)</del> <u>(SEQ</u>

**Table 5**  
**PCR Primers Used for the Generation of a Glycosylation**  
**Mutant of the Heavy Chain Variable Region of 5E8**

Sal I -20 -19 -18 -17 -16

MB 1650 5' ACA GAC CCG TCG ACC ATG GAG TTT GGG CTG 3' ~~(SEQ ID NO: 32)~~ (SEQ ID NO: 36)

Nhe I

118 117 116 115 114 113 112 111 110

MB 1651 5' CCC CTT GGT GCT AGC TGA GGA GAC GGT 3' ~~(SEQ ID NO: 33)~~ (SEQ ID NO: 37)

71 72 73 74 75 76 77 78 79

MB 1653 5' AGA GAG AAC GCC AAG AAC ACA CTG TTT 3' ~~(SEQ ID NO: 34)~~ (SEQ ID NO: 38)

79 78 77 76 75 74 73 72 71  
MB 1654 5' AAA CAG TGT GTT CTT GGC GTT CTC TCT 3' ~~(SEQ ID NO: 35)~~ (SEQ ID  
NO: 39)

Please delete the sequence listing beginning at page 89 of the specification (in its entirety), which was amend on July 25, 2000, to include the sequence listing filed on that day, and in place thereof insert the sequence listing submitted herewith.

Amendments To The Claims

1-41. (Cancelled)

*in pencil  
-amendments  
proposed by  
examiner  
06-28-04  
JBM*

... (Currently amended) A chimeric anti-human CD23 antibody wherein the light chain consists of the ~~variable domain~~ polypeptide encoded by nucleotides SEQ ID NO: 1, the heavy chain variable domain consists of the ~~variable domain~~ polypeptide SEQ ID NO: 2 nucleotides 48-423 of SEQ ID NO:3, and the constant region selected from the group consisting of human gamma-1 and gamma-3 regions.

*chimeric 58*

... (Previously presented) The anti-human CD23 antibody of claim 42 wherein the human constant region is a human gamma-1 constant region.

*chimeric*

... (Previously presented) The anti-human CD23 antibody of claim 42 wherein the human constant region is a human gamma-3 constant region.

45. (Currently amended) A composition containing ~~an~~ the chimeric anti-human CD23 antibody according to claim 42 and a pharmaceutically acceptable carrier.

*chimeric*

46. (Currently amended) A composition containing ~~an~~ the chimeric anti-human CD23 antibody according to claim 43 and a pharmaceutically acceptable carrier.

*chimeric*

47. (Currently amended) A composition containing ~~an~~ the chimeric anti-human CD23 antibody according to claim 44 and a pharmaceutically acceptable carrier.

*chimeric*

48. (Currently amended) A chimeric anti-human CD23 antibody wherein the light chain variable domain consists of the ~~variable domain~~ polypeptide encoded by nucleotides 67-387 of SEQ ID NO: 5, the heavy chain variable domain consists of the ~~variable domain~~ polypeptide encoded by nucleotides 58-411 of SEQ ID NO: 4 nucleotides 58-411 of SEQ ID NO: 7, and the constant region is a human constant region selected from the group consisting of a human gamma-1 constant region and a human gamma-3 constant region.

49. (Currently amended) A chimeric anti-human CD23 antibody wherein the light chain variable domain consists of the variable domain polypeptide encoded by SEQ ID NO: 3 nucleotides 67-387 of SEQ ID NO: 5 and the heavy chain variable domain consists of the variable domain polypeptide encoded by SEQ ID NO: 4 nucleotides 58-411 of SEQ ID NO: 7 with the exception that the asparagine codon encoded by nucleotides 289-291 of SEQ ID NO: 4 SEQ ID NO: 7 is replaced with a lysine codon. *and the constant region is a human constant region selected from the group consisting of a human gamma-1 constant region and a human gamma-2 constant region*

50. (Currently amended) The <sup>chimeric</sup> anti-human CD23 antibody according to claim 48 which comprises wherein the human constant region is a human gamma-1 constant region. *constant region selected from the group consisting of a human gamma-1 constant region and a human gamma-2 constant region*

51. (Currently amended) The <sup>chimeric</sup> anti-human CD23 antibody according to claim 48 which comprises wherein the human constant region is a human gamma-3 constant region.

52. (Currently amended) The <sup>chimeric</sup> anti-human CD23 antibody according to claim 49 which comprises wherein the human constant region is gamma-1 constant region.

53. (Previously presented) The <sup>chimeric</sup> anti-human CD23 antibody according to claim 49 which comprises a human gamma-3 constant region.

54. (Currently amended) A composition comprising an the <sup>chimeric</sup> anti-human CD23 antibody according to claim 48 and a pharmaceutically acceptable carrier.

55. (Currently amended) A composition comprising an the <sup>chimeric</sup> anti-human CD23 antibody according to claim 49 and a pharmaceutically acceptable carrier.

56. (Currently amended) A composition comprising an the <sup>chimeric</sup> anti-human CD23 antibody according to claim 50 and a pharmaceutically acceptable carrier.

57. (Currently amended) A composition comprising an the <sup>chimeric</sup> anti-human CD23 antibody according to claim 51 and a pharmaceutically acceptable carrier.

58. (Currently amended) A composition comprising ~~an~~ <sup>the</sup> anti-human CD23 antibody according to claim 52 and a pharmaceutically acceptable carrier. *chimeric*

59. (Currently amended) A composition comprising ~~an~~ <sup>the</sup> anti-human CD23 antibody according to claim 53 and a pharmaceutically acceptable carrier. *chimeric*

60. (Canceled)

61. (Previously presented) The composition of claim 45, which composition is a pharmaceutical composition.

62. (Previously presented) The composition of claim 46, which composition is a pharmaceutical composition.

63. (Previously presented) The composition of claim 47, which composition is a pharmaceutical composition.

64. (Previously presented) The composition of claim 54, which composition is a pharmaceutical composition.

65. (Previously presented) The composition of claim 55, which composition is a pharmaceutical composition.

66. (Previously presented) The composition of claim 56, which composition is a pharmaceutical composition.

67. (Previously presented) The composition of claim 57, which composition is a pharmaceutical composition.

68. (Previously presented) The composition of claim 58, which composition is a pharmaceutical composition.

69. (Previously presented) The composition of claim 59, which composition is a pharmaceutical composition.

70-73. (Canceled)

**REMARKS**

**Status Summary**

The request for continued examination (RCE) filed on October 21, 2003, has been entered. Claims 42-59, 61-69, and 71-73 are pending in the application and were examined. Claims 42-59 and 54-59 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly indefinite. A notice to comply with requirements for applications containing nucleic acid and amino acid sequences was issued together with the official action.

Claims 42, 45-52, are amended and claims 71-73 are canceled. A substitute sequence listing, including a paper copy and a computer-readable copy, and the requisite statement pursuant to 37 C.F.R. 1.821(f) are submitted herewith. The specification and claims are amended to use sequence identifiers as in the substitute sequence listing and to incorporate language suggested by the examiner with respect to 35 U.S.C. § 112, second paragraph. Reconsideration in view of the claim amendments and following remarks is respectfully requested.

**Rejection of Claims Under 35 U.S.C. § 112, Second Paragraph**

Claims 42-59, 61-69 and 71-73 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly indefinite. The rejection is based on noted informalities in the claims.

Claims 42, 45-52 are amended to incorporate language substantially as suggested by the examiner. With respect to claims 42, 48, and 49, the second mention of "variable domain" has been replaced with language specifying the nucleotides comprising the variable domain to clarify that leader sequence of each of SEQ ID NOS: 1, 3, 5, and 7 is not included. Claims 71, 72, and 73 are canceled as duplicative of claims 42, 48, and 49, respectively. Claims 43-44, 53-59, 61-69, and 71-73 depend from the amended claims and are believed to fully comply with the requirements of 35 U.S.C. § 112, second paragraph. Based thereon, withdrawal of the rejection is respectfully requested.

**Notice to Comply with Requirements for Applications**

**Containing Nucleic Acid and Amino Acid Sequences**

A notice to comply with requirements for applications containing nucleic acid and amino acid sequences was issued together with the official action. The previously submitted sequence fails to comply with the relevant rules because the computer-readable format copy

of SEQ ID NO:4 has only 354 nucleotides whereas the paper copy shows SEQ ID NO:4 as consisting of 411 nucleotides. The computer-readable format copy erroneously included a truncated sequence.

A substitute sequence listing, including a paper copy and a computer-readable copy, and the requisite statement pursuant to 37 C.F.R. 1.821(f) are submitted herewith. The substitute sequence listing includes a total of 39 sequences whereas the amendment filed July 25, 2000, includes a total of 35 sequences. The 4 additional sequences arise due to the separate listing of the nucleotide and amino acid sequences of former SEQ ID NOs:1-4, which now correspond to the nucleotide sequences of SEQ ID NOs: 1, 3, 5, and 7, and the amino acid sequences of SEQ ID NOs:2, 4, 6, and 8. In addition, nucleotides 118-120 of the 6G5 heavy chain variable region, which were identified as "TGG" encoding tryptophan (Trp) in SEQ ID NO:4 of the sequence listing filed July 25, 2000, are identified as "TCC" encoding serine (Ser) in SEQ ID NO:7 of the substitute sequence listing submitted herewith. The amendment is made to correct a typographical error in preparation of the sequence listing. Support for the amendment can be found in the originally filed application at the last line of page 53 and the first line of page 54. No new matter is added.

The specification is amended to insert the instant sequence listing in place of the previously filed sequence listing. The specification and claims are amended to use sequence modifiers as in the substitute sequence listing submitted herewith.

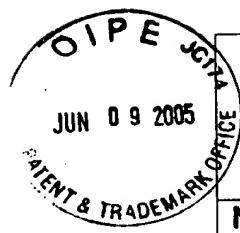
Conclusion

All rejections having been addressed, it is respectfully submitted that the present application is in condition for allowance and a notice to that effect is earnestly solicited. If any points remain in issue, which the examiner feels may be best resolved through a personal or telephone interview, he is kindly requested to contact the undersigned attorney at the telephone number listed below.

Respectfully submitted,  
PILLSBURY WINTHROP LLP

  
\_\_\_\_\_  
Thomas A. Cawley, Jr., Ph.D.  
Registration No. 40,944

*May 6*  
Date: April 28, 2004  
P.O. Box 10500  
McLean, VA 22102  
(703) 905-2144 Direct Dial  
(703) 905-2500 Facsimile  
TAC/JBM:ntb



Application No.

Applicant(s)

**Notice to Comply**Examiner  
Phuong N. HuynhArt Unit  
1644**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: It is noted that the computer copy of SEQ ID NO: 4 has only 354 nucleotides. Both computer and paper copy of the sequence listing of SEQ ID NO: 4 should have been 411 nucleotides.

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**



SEQUENCE LISTING

<110> REFF, MITCHELL E.  
KLOETZER, WILLIAM S.  
NAKAMURA, TAKEHIKO

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS

<130> 037003-0275470

<140> 09/019,441  
<141> 1998-02-05

<150> 08/803,085  
<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

<210> 1  
<211> 390  
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<213> Artificial Sequence

<220>

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<220>

<221> misc\_feature  
<222> (1)..(57)  
<223> leader sequence

<220>

<221> mat\_peptide  
<222> (58)..(390)

<220>

<221> CDS  
<222> (1)..(390)

<400> 1

atg gcc tgg act ctg ctc ctc gtc acc ctc ctc act cag ggc aca gga 48  
Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly  
-15 -10 -5

tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct 96  
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt 144  
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc	192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	
ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct	240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	
gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile	
65 70 75	
tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat	336
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr	
80 85 90	
aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc	384
Thr Thr Ser Ser Thr Leu Phe Gly Arg Gly Thr Arg Leu Thr Val	
95 100 105	
cta ggt	390
Leu Gly	
110	

<210> 2  
<211> 130  
<212> PRT  
<213> Artificial Sequence

<220>

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<400> 2

Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly  
-15 -10 -5

Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala  
30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser  
50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile  
65 70 75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr  
80 85 90

Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val  
95 100 105

Leu Gly  
110

<210> 3  
<211> 423  
<212> DNA  
<213> Artifical Sequence

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<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<220>  
<221> misc\_feature  
<222> (1)..(57)  
<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(423)

<220>  
<221> CDS  
<222> (1)..(423)

<400> 3

atg	aaa	cac	ctg	tgg	ttc	ttc	ctc	ctc	ctg	gtg	gca	gct	ccc	aga	tgg	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
																-5
																-15
																-10

gtc	ctg	tcc	cag	ctg	cag	ctg	cag	gag	tcg	ggc	cca	gga	gtg	gtg	aag	96
Val	Leu	Ser	Gln	Leu	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Val	Val	Lys	
																-1
																5
																10

cct	tcg	gag	acc	ctg	tcc	ctc	acc	tgc	gct	gtc	tct	ggt	ggc	tct	gtc	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Val	
																15
																20
																25

agc	agt	agt	aac	tgg	tgg	acc	tgg	atc	cgc	cag	ccc	cca	ggg	aag	gga	192
Ser	Ser	Ser	Asn	Trp	Trp	Thr	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	
																30
																35
																40
																45

ctg	gag	tgg	att	gga	cgt	atc	tct	ggt	agt	ggt	ggg	gcc	acc	aac	tac	240
Leu	Glu	Trp	Ile	Gly	Arg	Ile	Ser	Gly	Ser	Gly	Gly	Ala	Thr	Asn	Tyr	
																50
																55
																60

aac	ccg	tcc	ctc	aag	agt	cga	gtc	atc	att	tca	caa	gac	acg	tcc	aag	288
Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Ile	Ile	Ser	Gln	Asp	Thr	Ser	Lys	
																65
																70
																75

aac	cag	ttc	tcc	ctg	aac	ctg	aac	tct	gtg	acc	gcc	gcg	gac	acg	gcc	336
Asn	Gln	Phe	Ser	Leu	Asn	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
																80
																85
																90

gtg	tat	tac	tgt	gcc	aga	gat	tgg	gcc	caa	ata	gct	gga	aca	acg	cta	384
Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Trp	Ala	Gln	Ile	Ala	Gly	Thr	Thr	Leu	
																95
																100
																105

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca  
Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

423

<210> 4  
<211> 141  
<212> PRT  
<213> Artifical Sequence

<220>  
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<400> 4

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Leu Gln Leu Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Ala Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 5  
<211> 387  
<212> DNA  
<213> Artifical Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<220>  
<221> misc\_feature  
<222> (1)..(66)  
<223> leader sequence

<220>

<221> mat\_peptide  
<222> (67)..(387)

<220>  
<221> CDS  
<222> (1) .. (387)

<400> 5

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 -20 -15 -10

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96  
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
-5 -1 1 5 10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144  
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
15 20 25

cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192  
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
30 35 40

```

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
          45          50          55

```

```
cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
          60          65          70
```

```
gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
    75          80          85          90
```

gtt tat agt acc cct cg<sup>g</sup> acg ttc ggc caa ggg acc aag gtg gaa atc 384  
 Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 95 100 105

aaa  
Lys 387

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<210> 6
<211> 129
<212> PRT
<213> Artifical Sequence
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<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old  
World Monkey (macaque); leader sequence is an artificial sequence to  
facilitate cloning

<400> 6

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
-20 -15 -10

Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

$$-5 \qquad \qquad \qquad -1 \qquad 1 \qquad \qquad \qquad 5 \qquad \qquad \qquad 10$$

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
15 20 25

Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
30 35 40

Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val  
45 50 55

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
60 65 70

Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Tyr Cys Leu Gln  
75 80 85 90

Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
95 100 105

Lys

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<210> 7
<211> 411
<212> DNA
<213> Artifical Sequence
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<220>

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<220>
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<222> (1)..(57)
<223> leader sequence
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<220>  
<221> mat\_peptide  
<222> (58)..(411)

<220>  
<221> CDS  
<222> (1)..(411)

<400> 7

atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt cct ctt ttg aaa ggt 48  
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15 -10 -5

```

gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag 96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
          -1   1           5           10

```

cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc 144  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe  
15 20 25

acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag	192
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln	
30 35 40 45	
ggg ctg gag tgg gtc tca cgt att agt agt ggt gat ccc aca tgg	240
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp	
50 55 60	
tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc	288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala	
65 70 75	
aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg	336
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90	
gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc	384
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly	
95 100 105	
cag gga gtc ctg gtc acc gtc tcc tca	411
Gln Gly Val Leu Val Thr Val Ser Ser	
110 115	

<210> 8  
<211> 137  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 8

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys  
-1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe  
15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln  
30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp  
50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala  
65 70 75

Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
80 85 90

Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly  
95 100 105

Gln Gly Val Leu Val Thr Val Ser Ser  
110 115

<210> 9  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 9  
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<210> 10  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 10  
atcacagatc tctcaccatg aggctccctg ctcag 35

<210> 11  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
atcacagatc tctcaccatg gaarccccag ckcaag 35

<210> 12  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
atcacagatc tctcaccatg gtgttgacaga cccaggtc 38

<210> 13  
<211> 32  
<212> DNA  
<213> Artificial Sequence

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Attorney Ref. No. 037003-0275470

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13

ggtgtcagcca ccgttagcttt gatytccasc tt

32

<210> 14  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14

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34

<210> 15  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 15

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34

<210> 16  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 16

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35

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17

cttgggctga cctaggacgg t

21

<210> 18  
<211> 30

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18

gcgactaagt cgaccatgga ctggacctgg

30

<210> 19  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19

gcgactaagt cgaccatgaa acacacctgtgg

30

<210> 20  
<211> 33  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 20

gcgactaagt cgaccatgga gtttggctg agc

33

<210> 21  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 21

gcgactaagt cgaccatggg gtcaaccgcc atc

33

<210> 22  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 22

gcgactaagt cgaccatgtc tgtctccttc ctc

33

<210> 23  
<211> 46  
<212> DNA  
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<220>  
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<400> 23

gccaggggga agaccgatgg gcccttggtg ctagctgagg agacgg

46

<210> 24  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 24

gatggccct tggtgctagc tgaggagacg g

31

<210> 25  
<211> 51  
<212> DNA  
<213> Artificial Sequence

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<400> 25

ggtgctagct gaggagacgg tgaccaggac tccctggccc cagaaggcta g

51

<210> 26  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26

atttaggtga cactata

17

<210> 27  
<211> 16  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 27

gttttcccag tcacg

16

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28

atatacgact cactatagg

20

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

ccgtcagatc gcctggagac gcc

24

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gcagttccag atttcaactg

20

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ccaggccact gtcacggctt c

21

<210> 32

<211> 20

<212> DNA

U.S. Application No. 09/019,441  
Attorney Ref. No. 037003-0275470

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

cagagctggg tacgtcctca

20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

gcccccagag gtgctttgg

20

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

acacagaccc gtcgacatgg

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<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

gctctcgag gtgctcctgg

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<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

acagaccgt cgaccatgga gtttggctg

30

<210> 37  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 37

cccccgttgtg ctagctgagg agacgg

27

<210> 38  
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<223> Description of Artificial Sequence: Primer

<400> 38

agagagaacg ccaagaacac actgttt

27

<210> 39  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 39

aaacagtgtg ttcttggcgt tctctct

27

SEQUENCE LISTING

<110> REFF, MITCHELL E.  
KLOETZER, WILLIAM S.  
NAKAMURA, TAKEHIKO

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE  
THEREOF AS THERAPEUTICS

<130> 037003-0275470

<140> 09/019,441  
<141> 1998-02-05

<150> 08/803,085  
<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

<210> 1  
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World Monkey (macaque); leader sequence is an artificial sequence to  
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<220>  
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<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(390)

<220>  
<221> CDS  
<222> (1)..(390)

<400> 1

atg gcc tgg act ctg ctc ctc gtc acc ctc ctc act cag ggc aca gga 48  
Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly  
-15 -10 -5

tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct 96  
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt 144  
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc	192
Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala	
30 35 40 45	
ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct	240
Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser	
50 55 60	
gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile	
65 70 75	
tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat	336
Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr	
80 85 90	
aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc	384
Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val	
95 100 105	
cta ggt	390
Leu Gly	
110	

<210> 2  
<211> 130  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 2

Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly  
-15 -10 -5

Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser  
-1 1 5 10

Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val  
15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala  
30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser  
50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile  
65 70 75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr  
80 85 90

Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val  
95 100 105

Leu Gly  
110

<210> 3  
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<212> DNA  
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<220>  
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<220>  
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<222> (1)..(57)  
<223> leader sequence

<220>  
<221> mat\_peptide  
<222> (58)..(423)

<220>  
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<222> (1)..(423)

<400> 3

atg aaa cac ctg tgg ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

gtc ctg tcc cag ctg cag ctg cag gag tcg ggc cca gga gtg gtg aag 96  
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc 144  
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga 192  
Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac 240  
Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Ala Thr Asn Tyr  
50 55 60

aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag 288  
Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc 336  
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta 384  
Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca  
Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

423

<210> 4  
<211> 141  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 4

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val  
15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys  
65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu  
95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 5  
<211> 387  
<212> DNA  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (1)..(66)  
<223> leader sequence

<220>

<221> mat\_peptide  
<222> (67)..(387)

<220>  
<221> CDS  
<222> (1)..(387)

<400> 5

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg 48  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
-20 -15 -10

ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96  
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
-5 -1 1 5 10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144  
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
15 20 25

cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192  
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
30 35 40

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240  
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val  
45 50 55

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288  
Pro Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
60 65 70

gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336  
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
75 80 85 90

gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc 384  
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
95 100 105

aaa 387  
Lys

<210> 6  
<211> 129  
<212> PRT  
<213> Artifical Sequence

<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old  
World Monkey (macaque); leader sequence is an artificial sequence to  
facilitate cloning

<400> 6

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp  
-20 -15 -10

Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

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<210> 7
<211> 411
<212> DNA
<213> Artifical Sequence
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<220>  
<223> Description of Artificial Sequence: Mature peptide is derived from Old  
World Monkey (macaque); leader sequence is an artificial sequence to  
facilitate cloning

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<220>
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<223> leader sequence
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<220>  
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<222> (58)..(411)

<220>  
<221> CDS  
<222> (1)...(411)

<400> /

atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt cct ctt ttg aaa ggt 48  
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15 -10 -5

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gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag 96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
          -1      1          5          10

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cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
15          20          25

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acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag	192
Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln	
30 35 40 45	
ggg ctg gag tgg gtc tca cgt att agt agt ggt gat ccc aca tgg	240
Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp	
50 55 60	
tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc	288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala	
65 70 75	
aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg	336
Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr	
80 85 90	
gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc	384
Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly	
95 100 105	
cag gga gtc ctg gtc acc gtc tcc tca	411
Gln Gly Val Leu Val Thr Val Ser Ser	
110 115	

<210> 8  
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<212> PRT  
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<220>  
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<400> 8

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly  
-15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Ala Lys  
-1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe  
15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln  
30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Gly Asp Pro Thr Trp  
50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala  
65 70 75

Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
80 85 90

Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly  
95 100 105

Gln Gly Val Leu Val Thr Val Ser Ser  
110 115

<210> 9  
<211> 41  
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<220>  
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<400> 9  
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<210> 10  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 10  
atcacagatc tctcaccatg aggctccctg ctcag 35

<210> 11  
<211> 35  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
atcacagatc tctcaccatg gaarccccag ckcag 35

<210> 12  
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<212> DNA  
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<220>  
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<400> 12  
atcacagatc tctcaccatg gtgttgcaga cccaggtc 38

<210> 13  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 13

ggtgtcagcca ccgttagcttt gatytccasc tt

32

<210> 14  
<211> 34  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 14

atcacagatc tctcaccatg rcctgstccc ctct

34

<210> 15  
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<400> 15

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34

<210> 16  
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<400> 16

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35

<210> 17  
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<400> 17

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21

<210> 18  
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<212> DNA  
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<400> 18

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30

<210> 19  
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<212> DNA  
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<220>  
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<400> 19

gcgactaagt cgaccatgaa acacctgtgg

30

<210> 20  
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<400> 20

gcgactaagt cgaccatgga gtttgggctg agc

33

<210> 21  
<211> 33  
<212> DNA  
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<400> 21

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33

<210> 22  
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<212> DNA  
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<220>  
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<400> 22

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33

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<210> 23  
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46

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<220>  
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31

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ggtgctagct gaggagacgg tgaccaggac tccctggccc cagaaggcta g

51

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<212> DNA  
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<220>  
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<400> 26

attaggtga cactata

17

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gttttcccag tcacga

16

<210> 28

<211> 20

<212> DNA

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20

<210> 29

<211> 24

<212> DNA

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24

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ccaggccact gtcacggctt c

21

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<210> 35

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<210> 36

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27